Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for determining the presence or absence of *Mycobacterium tuberculosis* (*M. tuberculosis*) in a biological sample, comprising

(a) amplifying a DNA segment using the nucleic acids from the biological sample as a template and a primer pair, wherein the amplified DNA segment comprises ~~capable of amplifying~~ a region of SEQ ID NO: 1 that encompasses position -215, in the 5' to 3' direction of reading, upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon, and

(b) determining the presence or absence of the polymorphism specific for *M. tuberculosis* in position -215, in the 5' to 3' direction of reading, upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon, wherein the presence of the polymorphism indicates the presence of *M. tuberculosis* in the biological sample, and the absence of the polymorphism indicates the absence of *M. tuberculosis* in the biological sample.

2. (Currently Amended) The method according to claim 1, wherein step (a) is carried out by polymerase chain reaction (PCR), nucleic acid sequence based amplification (NASBA), strand displacement amplification (SDA) or ligase chain reaction (LCR).

3. (Previously Presented) The method according to claim 2, wherein the PCR is a real time PCR.

4. (Currently Amended) The method according to any one of claims 1 to 3, wherein step (b) is carried out by ~~hybridisation~~hybridization of one or several probes.

5. (Previously Presented) The method according to any one of claims 1 to 3, wherein the DNA segment of step (a) has a length of 1 to 500 nucleotides.

6. (Previously Presented) The method according to any one of claims 1 to 3, wherein the DNA segment of step (a) has a length of 1 to 300 nucleotides.

7. (Previously Presented) The method according to any one of claims 1 to 3, wherein the DNA segment of step (a) has a length of 1 to 155 nucleotides.

8. (Previously Presented) The method according to any one of claims 1 to 3, wherein one primer of the primer pair of step (a) comprises SEQ ID NO: 2 or SEQ ID NO: 3.

9. (Currently Amended) The method according to any one of claims 1 to 3, wherein step (b) is carried out by means of at least one pair of labeled ~~hybridisation~~hybridization probes, one probe being labeled at its 3' end and the other probe being labeled at its 5' end, and the probes binding specifically to the DNA segment of step (a) in such a way that a fluorescence resonance energy transfer (FRET) is made possible.

10. (Currently Amended) The method according to claim 9, wherein one probe of the probe pair comprises SEQ ID NO: 4 and the other probe comprises SEQ ID NO:5; one probe of the probe pair comprises the complementary sequence of SEQ ID NO:4, and the other probe comprises the complementary sequence of SEQ ID NO:5; one probe of the probe pair comprises SEQ ID NO: 4 and the other probe comprises SEQ ID NO:6; or one probe of the probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe comprises the complementary sequence of SEQ ID NO:6.

11. (Previously Presented) The method according to any one of claims 1 to 3, wherein the sample is a clinical sample selected from the group consisting of saliva, bronchial lavage, gastric juice, urine, faeces, liquor, bone marrow, blood and biopsies.

12.-18. (Canceled)

19. (Currently Amended) A ~~hybridisation~~hybridization probe for detecting the polymorphism specific for *M. tuberculosis* located in position -215 in the 5' to 3' direction of reading upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon.

20. (Currently Amended) A ~~hybridisation~~hybridization probe pair for detecting the polymorphism specific for *M. tuberculosis* located in position -215 in the 5' to 3' direction of reading upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon.

21. (Currently Amended) The ~~hybridisation~~hybridization probe pair according to claim 20, wherein one probe of the probe pair comprises SEQ ID NO: 4 or the complementary sequence thereof.

22. (Currently Amended) The ~~hybridisation~~hybridization probe pair according to claim 20, wherein one probe of the probe pair comprises SEQ ID NO: 5 or the complementary sequence thereof.

23. (Currently Amended) The ~~hybridisation~~hybridization probe pair according to claim 20, wherein one probe of the probe pair comprises SEQ ID NO: 6 or the complementary sequence thereof.

24. (Currently Amended) The ~~hybridisation~~hybridization probe pair according to claim 20, wherein one probe in the probe pair comprises SEQ ID NO: 4 and the other probe comprises SEQ ID NO: 5, or one probe in the probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe comprises the complementary sequence of SEQ ID NO:5.

25. (Currently Amended) The ~~hybridisation~~hybridization probe pair according to claim 20, wherein one probe in the probe pair comprises SEQ ID NO: 4 and the other probe

comprises SEQ ID NO: 6, or one probe in the probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe comprises the complementary sequence of SEQ ID NO:6.

26. (Currently Amended) A ~~hybridisation~~hybridization probe comprising SEQ ID NO: 4 or the complementary sequence thereof.

27. (Currently Amended) A ~~hybridisation~~hybridization probe comprising SEQ ID NO: 5 or the complementary sequence thereof.

28.-30. (Canceled)

31. (Currently Amended) A kit for detecting *M. tuberculosis*, comprising:

at least one primer pair suitable for amplifying a DNA segment from SEQ ID NO: 1, wherein the DNA segment comprises position -215 in the 5' to 3' direction of reading upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon, or

at least one ~~hybridisation~~hybridization probe or a ~~hybridisation~~hybridization probe pair suitable for detecting the polymorphism specific for *M. tuberculosis* located in position -215 in the 5' to 3' direction of reading upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon.

32. (Currently Amended) The kit according to claim 31, wherein one primer of the primer pair comprises SEQ ID NO:2 and the other primer comprises SEQ ID NO:3 ~~is the primer pair according to claim 15~~.

33. (Currently Amended) The kit according to claim 31, wherein

(a) one probe in the ~~hybridisation~~hybridization probe pair ~~is the probe pair according to claim 24 or claim 25~~ comprises SEQ ID NO:4 and the other probe in the probe pair comprises SEQ ID NO:5;

(b) one probe in the hybridization probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe in the probe pair comprises the complementary sequence of SEQ ID NO:5;

(c) one probe in the hybridization probe pair comprises SEQ ID NO:4 and the other probe in the probe pair comprises SEQ ID NO:6;

(d) one probe in the hybridization probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe in the probe pair comprises the complementary sequence of SEQ ID NO:6.

34. (Currently Amended) The kit according to claim 33, ~~further comprising the primer pair according to claim 15~~ wherein one primer of the primer pair comprises SEQ ID NO:2 and the other primer of the primer pair comprises SEQ ID NO:3.

35. (Previously Presented) The kit according to claim 31 or claim 32, further comprising reagents or auxiliary agents necessary or useful for carrying out a nucleic acid amplification or detection reaction.

36. (Currently Amended) A method for determining the presence or absence of ~~*mycobacterium*~~ *Mycobacterium tuberculosis* (*M. tuberculosis*) in clinical material, comprising

a) extracting microbial DNA from clinical material,

b) amplifying from the extracted DNA at least one DNA fragment of the promoter region of the *narGHJI* nitrate reductase operon of mycobacteria containing at least one DNA polymorphism specific for *M. tuberculosis*, and

c) determining the presence or absence of the specific ~~hybridisation~~hybridization of the DNA fragment of step (b) by way of melting curve analysis with at least one ~~hybridisation~~hybridization probe that comprises the nucleotide sequence selected from the group consisting of SEQ ID NO: 5, the complementary sequence to SEQ ID NO: 5, SEQ ID NO: 6, and the complementary sequence to SEQ ID NO: 6, wherein the presence of the specific hybridization indicates the presence of *M. tuberculosis* in the clinical material,

and the absence of the specific hybridization indicates the absence of *M. tuberculosis* in the clinical material.

37. (Currently Amended) The method according to claim 36, wherein the specific hybridization is based on the DNA polymorphism located in position -215 of the promoter region, in the 5' to 3' direction of reading, upstream of the translation start codon GTG of the *narGHJI* nitrate reductase operon.

38. (Currently Amended) The method according to claim 37, wherein step b) is carried out by means of a primer pair having one primer that comprises SEQ ID NO: 2 and the other primer comprises SEQ ID NO: 3.

39. (Currently Amended) The method according to any one of claims 36 to 38, wherein step c) is carried out with at least one pair of labeled ~~hybridisation~~hybridization probes, and wherein one probe of the pair comprises SEQ ID NO: 4 and the other probe comprises SEQ ID NO: 5, one probe of the pair comprises the complementary sequence of SEQ ID NO:4 and the other probe comprises the complementary sequence of SEQ ID NO:5, one probe of the pair comprises SEQ ID NO:4 and the other probe comprises SEQ ID NO:6, or one probe of the pair comprises the complementary sequence of SEQ ID NO: 4 and the other probe comprises the complementary sequence of SEQ ID NO: 6.

40. (Previously Presented) The method according to any one of claims 36 to 38, wherein step (b) is carried out by polymerase chain reaction (PCR).

41. (Previously Presented) The method according to any one of claims 36 to 38, wherein step (c) is carried out during or after step (b).

42. (Previously Presented) The method according to any one of claims 36 to 38, wherein step (c) is carried out via real time PCR.

43. (Currently Amended) The method according to any one of claims 36 to 38, wherein step (c) is carried out by fluorescence detection, and the labeled ~~hybridisation~~hybridization probe pairs are formed as fluorescence resonance energy transfer (FRET) pair.

44. (Previously Presented) The method according to any one of claims 36 to 38, wherein the clinical material is selected from the group of clinical samples consisting of saliva, bronchial lavage, gastric juice, urine, faeces, liquor, bone marrow, blood and biopsies.

45. (Canceled)

46. (Currently Amended) An oligonucleotide which ~~hybridises~~ hybridizes specifically with an *M. tuberculosis*-specific promoter region of the *narGHJI* nitrate reductase operon, comprising SEQ ID NO: 5 or the complementary sequence thereof.

47. (Currently Amended) An oligonucleotide which ~~hybridises~~ hybridizes specifically with an *M. tuberculosis*-specific promoter region of the *narGHJI* nitrate reductase operon, comprising the nucleotide sequence SEQ ID NO: 6 or the complementary sequence thereof.

48. (Currently Amended) An oligonucleotide pair, wherein one oligonucleotide in the pair comprises SEQ ID NO: 4 and the other oligonucleotide comprises SEQ ID NO: 5, or one oligonucleotide in the pair comprises the complementary sequence of SEQ ID NO:4 and the other oligonucleotide comprises the complementary sequence of SEQ ID NO:5.

49. (Currently Amended) An oligonucleotide pair, wherein one oligonucleotide in the pair comprises SEQ ID NO: 4 and the other comprises SEQ ID NO: 6, or one oligonucleotide in the pair comprises the complementary sequence of SEQ ID NO:4 and the other comprises the complementary sequence of SEQ ID NO:6.

50. (Currently Amended) A kit for detecting *Mycobacterium tuberculosis* comprising

a) at least one primer pair, wherein one primer in the primer pair comprises SEQ ID NO: 2, and the other primer comprises SEQ ID NO: 3 and

b) at least one ~~hybridisation~~hybridization probe pair, wherein one probe in the probe pair comprises SEQ ID NO: 4 and the other probe comprises SEQ ID NO: 5, one probe in the probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe comprises the complementary sequence of SEQ ID NO:5, one probe in the probe pair comprises SEQ ID NO: 4 and the other probe comprises SEQ ID NO: 6, or one probe in the probe pair comprises the complementary sequence of SEQ ID NO:4 and the other probe comprises the complementary sequence of SEQ ID NO:6.

51. (Previously Presented) The method of claim 36, wherein the at least one hybridization probe in step (c) comprises SEQ ID NO: 6 or the complementary sequence thereof.

52. (New) The method according to claim 1, wherein one primer of the primer pair of step (a) comprises SEQ ID NO:2.

53. (New) The method according to claim 1, wherein one primer of the primer pair of step (a) comprises SEQ ID NO:3.

54. (New) The method according to claim 1, wherein one primer of the primer pair of step (a) comprises SEQ ID NO:2 and the other primer comprises SEQ ID NO:3.